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Page

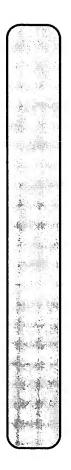
> 0 < of the of

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file sq2nsq.res made by on Tue 11 Apr 95 9:41:17-PDT.

Query sequence being compared:US-08-223-263-2 (1-1795)
Number of sequences searched: 57621
Number of scores above cutoff: 4210 Results of the initial comparison of US-08-223-263-2 (1-1795) with: Data bank : N-GeneSeq 17, all entries

1000-* 100-500-



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PARAMETERS

	Initial scores to save Optimized scores to save	Similarity matrix Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group
SEA	45 re 0	Unitary 1 1.00 0.33 5 0
SEARCH STATISTICS	Alignments to save Display context	K-tuple Joining penalty Window size
	15 10	4 30 32

Scores: CPU 00:07:14.98 Mean 20 Total Elapsed 00:07:16.00 Standard Deviation 15.15

Number of residues: Number of sequences searched: Number of scores above cutoff: 24347505 57621 4210

Cut-off raised to 12.
Cut-off raised to 20.
Cut-off raised to 29.
Cut-off raised to 35.
Cut-off raised to 39.
Cut-off raised to 44.
Cut-off raised to 48.

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

**** 9 standard deviations above mean **** 1. Q03259 Pseudorabies virus glycoprote 4897 162 730 **** 8 standard deviations above mean **** 2. Q27816 Adrenalin receptor subtype be 1398 150 620	Sequence Name Description Length Score Score Sig. Frame
** 730 ** 620	ore
9.37 0 8.58 0	Sig. Frame

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118. 119. 119. 220. 221. 222. 223. 224. 225. 225. 226. 227. 227. 330. 331. 331. 331. 331. 331. 331. 331	3. 4. 5. 6. 7. 110. 111. 113. 114.
N30043 Q13332 N60292 N60292 N30044 Q04781 Q24321 Q24012 Q24012 Q24013 Q24011 N60294 Q22696 N90501 N60274 N81271 Q56908 Q4677 Q45995 Q46889 Q26689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q2689 Q26	047834 003684 005748 005749 023729 023729 023682 029260 029260 029260 026470 024675 024675 024675 024322
Sequence encoding bovine leuk GDP-Fuc:beta-D-galactoside al Intron free glucoamylase stru Mouse tumour necrosis factor Sequence encoding bovine leuk Sequence encoding Ty3 positio Mutant thermostable DNA polym C-terminal of glucoamylase ge Gal alpha-2,6-ST (clone 14). **** 5 standard deviations a Goat growth hormone precursor Sequence encoding creatine am Sequence encoding creatine am DNA encoding dylocosyltransf Encodes MPIV env-mpl fusion IDNA - exons III to XIV. VAC-beta (genomic - part A). VAC-beta (genomic - part A). DNA sequence of gene encoding 5' UTR of ELAM1 from clone EL Proteinase 3 coding sequence. VNTR locus D20S15 flanking re Encodes recombinant human lys Sequence encoding human bone DNA encoding tumour associate Sequence encoding a jumunore Sequence encoding a ju	01
1182 8174 2016 3500 1150 1150 1150 1150 1150 2370 2277 2277 1755 1755 1755 1756 1712 1712 1712 1712 1713 1714 1714 1716 1716 1716 1716 1716 1716	above mean 2281 2281 1883 1883 582 711 711 711 711 711 711 711 711 711 71
114 113 113 113 112 112 112 112 111 111 111	134 134 133 133 133 132 132 132 132 132 132 132
769 769 769 769 769 769 769 760 760 760 760 760 760 760 760 760 760	667 667 653 6241 2241 2259 2259 2368 752 752 752 753 751 751
5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.	
000000000000000000000000000000000000000	

PT SKE DT AC US-08-223-263-2 (1-1795) Pseudorabies virus glycoprotein gII polypeptide. Aujeszky's disease; vaccine; herpes virus; pig; ss. Pseudorabies virus. Q03259 standard; DNA; 4897 BP. Q03259; /*tag= 22-JUL-1990 (first entry) Pseudorabies virus glycoprotein gII polypeptide Location/Qualifiers 2639..3001

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4

Residue Identity = Gaps = Initial Score 390 | 340 | 340 | 350 | 360 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 370 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 | 380 430 440 450 CCTGTCC---TGCTGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATG--GAGGAGACCAAGG GGGAGCCACGCCAGCCAGACACCCCGGCCAGA---ATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCT 18-JUL-1989; 201887.
01-AUG-1988; EP-112479.
(ALKU) Akzo NV.
Schreurs CS, Mettemleiter TC, Simon AJ, Lukacs WPI; 90-038534/06.
P-PSDB; R03732. Sequence disease. Immunogenic polypeptide of pseudo-rabies virus for use in mammalian vaccine against Aujeszky's disease. Disclosure; Fig 1; 21pp; English.
The polypeptide may be used as a vaccine to provide 07-FEB-1990. EP-353809-A ---CCCATGAAGGCCCTGTACCCCGTCACGACGAAGACGCTCAAGGA----GGACGGCGTCGACGAG mammals, e.g. pigs, with resistance against Aujeszky's note="gII glycoprotein" 11 4897 BP; 3430 162 46% 202 3370 Optimized Score = Matches = 3310 Conservative Substitutions 594 A; 3440 280 3380 2052 C; 3320 3450 220 3390 290 1495 G; 756 T; 3330 3460 730 Significance 867 Mismatches Ž 300 3400 Rhiza 3340 3410 11 Ü, 3480 3350 9.37 778 0

Page

GAGC-T---CCCAAACAGGACTTCTGGATT--GTTGGAGACAAACTTCACTGCCTCAGCCAGAACTAC-TGG 600 610 620 630 640 650 660 CCTCCTTGGAACCCAGCCTTCCTCACAGGGCAGGACCACAGGCTCACAAGGATCCCAATGCCATC--TTCCT-GTCAGGC--GGGCCCCACCACCACAG---CTGTCCCCAGCAGAACCTCTCTAGTCC-TCACACT---GAAC 460 470 480 490 500 510 520 CACAGGACATTCTGGGAGCACTGATGGCAGCACGGGGACAACTGGGACCCA GATGGCCACGCCGCCGGCACT--ACCAGCGCCT-CGAG-AGCGAGGACCCCGACGCCCTGTAGCCC---C CTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGATTCCTGGTCTGCT--GAACCAAACCTCCAGG TCCCTGGACCAAATCC--CCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTC

2. US-08-223-263-2 (1-1795) Q27816 Adrenalin receptor subtype beta-1 gene

GCTGGGC-

CCTTTACTATCATTCTCAGTGGGACTCTGAGTCCCCATATTCTTAACAGATCTTTACTCTTGAGAAATG

-GGCGCGGAACGAGCCCGGACCCGGGACCGGAAGCTGGTGCGCATGC

CTTGAGTCAGAAAAC-AGAGAAAGGGTAATTTCCTTTGC-TTCAAATTCAAGGCCTTCCAACGCCCCCATCC

GCGGGGGTGCTGGTACACGT--4710 4720

ACTCATCAGAGCAGCTAGCTCTTTGGTC-TATTTTCTG---CAGAAATTTGCAACTCACTGATTCTCTACAT

AACGGGGGAAACCATACAACGGGGGTCCGCGGGGCCCTCACACGCGCCAGCTCTTGCGGCGCGACGC-GC

GGTGGCCGGTG-AGGTCGATGACGGGTCGGGGGTGCTGGTACAGGCCGTCG-TCCGCGCGCGG----GTCCGCGG

Residue Initial ATTCCTCACCCTTGGCCCGCCTTTGCCCCACCCTACTCTGCCCCAGAA--GTGCAAGAGCCTAAGCCGCTCC ATGGCCCCAG---GAAGGATTCAGGGGA--GAGGCCCAAACAGGGAAGCCCGAGCCAGACACCCCG-G The rat adrenalin receptor subtype beta 1 gene was obtd. by cloning of a rat genomic library which was screened with a probe derived from human adrenalin receptor subtype beta 1. The gene was introduced into a plasmid to obtain a recombinant DNA mol. (RGB-1). The DNA sequence was useful in studies of drugs acting on adrenalin receptor subclass beta 1, e.g. dobutamine or prenalterol, or drugs DNA encoding adrenalin receptor sub-type beta-1 - obtd. by cloning rat genome DNA library and rat cDNA library with derived from human adrenalin Claim 1; Page 5; 8pp; Japanese. (SUMU) SUMITOMO SEIYAKU WPI; 92-304939/37. 03-AUG-1992. 15-FEB-1991; 044479. 27-FEB-1990; JP-048794 Adrenalin receptor subtype beta-1 gene.
Drugs; dubutamine; prenalterol; acebutolol; metoprolol; atenolol; practolol; ss. blocking the receptor, e.g. acebutolol, metoprolol, P-PSDB; R26505 Q27816 standard; cDNA; 1398 Q27816; J04211374-A. 2-FEB-1993 (first entry) Identity Score ATGGGCGCGGGGGCG-CTCGCCCTGGCAA---CCT--GTCGTCGGC X 10 20 30 40 50 B 11 u 1398 160 BP; 150 50% 173 Conservative Substitutions Optimized Score = Matches = 184 A; 겆 ₽₽ 523 C; 180 620 748 442 G; 190 Mismatches Significance atenolol or 249 11 8.58 574

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490

TG-GAG----GGAGTGATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCT

CCA-ACCGGGCCTACGCCATCGCCTCGTCCGTCTCTCTACGTGCCCCTGTGCATCATGGCCTTCGTG



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US-08-223-263-2 (1-1795) Q47834 Murine inte Murine interleukin 9 receptor clone p9RC4.

Q47834 standard; cDNA; 228 Q47834; 16-MAR-1994 (first entry) 2281 BP.

Murine interleukin 9 receptor clone p9RC4.
Interleukin 9 receptor; IL-9; antibodies; therapy; probe; antagonist; ss
Mus musculus.

Location/Qualifiers 5..1411

/*tag= a
/product= Interleukin 9 receptor.
W09318047-A.

PPD PTT TEN 16-SEP-1993. 25-FEB-1993; U01720

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Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 210 220 230 240
ACGCCAGCAG-ACA--CCCCGGCCAGAATGGAGCTGACTGAATTGCTCCTCGTG-GT--CATG---
                                                              CATCAGCAGGCTCAGAGTC-
                                                                             CTTCGTGACTCCCA-TGTCCTTCACAGCAGACT--GAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCT
TCCTAACTGCA-AGGCTAACGCTGTCCAGCCCGGGCTCCTCCTGCTGAGCTCCGGAGTCCTCAGTAAACTG
                                                                                                                                                                                                                                         TCTTTTACCAGAACATTGCATCCCGAGGCGTTCTTCCATCCTTCTAC-AGTGTGTACCATGGGGACTTC 910 920 930 940 950 960 970
                                                                                                                                                                                                                                                                                                                                    GC-CCATCTTTCTTCTGCTGACTGGCTTTGTTCCACCTTCTGTTCAAG---CTGTCACCCAGGCTGAAGAGAA 840 850 800 900
                                                                                                                                                                                                                                                                                                                                                                              130 140 150 GCAAGAGCCTAAGCCGCCTCCATGGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CAGACTTGGACAGGGGCCCGCAG---AGCC--GGACCACAAGC--AAGACAGAATGGT-GTCAGT--ACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding interleukin-9 receptor - used to produce reagents used in diagnosis and therapy involving interleukin 9R Claim 6; Page 13; 30pp; English.

The interleukin (II) 9 receptor nucleic acid sequence can be used to produce II-9 receptor or as probes for cells which respond to the cytokine. The complementary sequences can be used to inhibit the expression of the II-9 receptor protein and to probe for the II-9 coding sequences. Transfected cell lines can be used to screen for II-9 receptor agonists and antagonists. Antibodies directed against the II-9 receptor can be used therapeutically to block II-9 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LUDW-) LUDWIG INST CANCER RES. Druez C, Renauld J, Van Snick WPI; 93-303390/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the receptor and for qualitative and quantative measurement of II-9 receptor levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-MAR-1992; US-847347
                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2281 BP;
                                                                                                             340
                                                                                                                                            990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
48%
242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Optimized Score = 667
Matches = 826
Conservative Substitutions
                                                           497 A;
                                                                                                             350
                                                                                                                                                                                                           280
                                                                                                                                            1000
                                                                                                                                                                                                                                                                                                                                                                    160 170 180 190
--CCCAGGAAGGATTCAGGGGGAGAGCC-CCCAAACAG-GGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          636 C;
                                                                                                                                                                                                           290
                                                                                                           360
                                                                                                                                            1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 G;
                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Significance = Mismatches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 T;
                                                                                                                                                                                                           310
                                                                                                                                            1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.52
630
0
                                                                                                                                                                                                                                                                       250
--CTTC
||||
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870 980 890

ACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGAT---ATTCT-CCTTCCCCAACCCATCCTCCTACTGGAC 1090

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TATTTTTAAG--CTATCAGCAATACTCATCAGAGCAGCTAGCTCTTTGGTCTATTTTCTGCAGAAATTTG

US-08-223-263-2 (1-1795) Q03684 pAT744 clone of gene encoding activated T cell mRN

Q03684 standard; DNA; 659 BP. Q03684;

12-SEP-1990 (first entry)
pAT744 clone of gene encoding activated T cell mRNAs.
Periferal blood mononuclear cell; PBMC; lymphokine;
cytokine; mitogen; ds.

Homo sapiens.

CDS Location/Qualifiers 74..349

FTH OK WE DET

/*tag=

US7312001-A.

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Residue Identity Initial 330 260 270 280 290 310 310 CTGCAAGGCTACCGCTGCCGGCTCCTGCTCTGCTTGGTGGCTCCGAGTCCTCAGTAAACTGCTTCGT GA-GCCCGGATGCTTCTCCATGAGACACATCTCCT--CCATA--CTCAGGACTCCTCTCCCCAGTTCCTG-T GTACGAGTATGAC-CTG--GAACTGAACT-GAGCTGCTCAGAAGA-CAGGAAGTCTTCAGGGAA-GGTCACCT 330 340 350 350 370 380 390 CCAGCTGTGGTATTCCAAACCAAAGAAGCAAGCAAGTCTGTGCTGGTTGCAGTGAATCCTGGGTC-CAGGA GC--CCTTCTCCACCCGGATAGATTCCTCACCCTTGG--CCCGCCTTTGCCCCACCCTACT-CTGCCCAGA-AGAAAACCTCTTTTCCACCAATACCATGAAGCTCTCCC-GTG-ACTGTCCTCTCTCTCCTCATG---CTAGTA
50 60 70 80 GACTCCCATGTCCTTC-ACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT CCAGC-CAGACA-CCCCGGCCA---GAATGGAGC-TGACTGAATTGCTCCTCGTG-GTCATGCTTCTCCTAA 130 140 150 160 170 180 190 AGTGCAAGAGACCCCCAAGAGAGACCCCCAAACAGGAACCACGCAAGAACAGGAATTCAAGGGAAGACCCCCAAACAGGGAGCCAAG ACCGCGAG----190 The lymphokine/cytokine-like proteins are associated with the inflammatory response and/or have mitogenic activities. Antigens raised to the proteins may be useful in detection and purification, especially in bloassays of various tumour cells or genetic defects in the inflammatory response. The best copy of the sequence available is still unclear and some errors in the sequence may occur. Sequence 659 BP; 161 A; 181 C; 124 G; 193 T; New lymphokine—cytokine genes - isolated using mRNA from activated mononuclear cells and T cells. Disclosure; 184pp; English 13-MAR-1990. 16-DEC-1988; JS-312001. 16-DEC-1988; US-312001. (USSH) US Dept Health & Human. Siebenlist U, Leonard WJ, Zipfel PJ, WPI; 90-139708/18. P-PSDB; R04222. 120 Score X TCTTCCTAC----130 (I II II 200 210 133 47% 68 140 10 -CCAT-CTGCTCCCCAGAGGGCTG-CCTG-CTGTGCACTTGGGTCCTGGA Matches = 302 Conservative Substitutions Optimized Score 210 80 360 150 220 90 human Irving 370 H II 160 periferal 30 251 302 230 SG, 100 380 Kelly Mismatches Significance 170 blood 40 ζ, 390 II 50 7.46 268 0 120

420

430

Initial Score

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Optimized Score

11

653

Significance

7.46

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US-08-223-263-2 (1-1795)
Q05748 EPO recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         610
CCAGCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 550 X CATCCCTCCTGG--GGCAGCTTTCTGGACAGGTCCGTCTCCTTGGGGGCCCTGCAGAGCCTCCTTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTTAGCCAAAGGATAACTCTCCCCTATG--GGGATGG-TCCACTG---TCACTGTTTCTCTCTGTTGCA
530 540 550 550 570
                                               Erythropoletin receptor and gene - used for developing reagents and systems to control and study erythropolesis.

Claim 7; Fig 2; 53pp; English.

The sequence was obtd. from a clone isolated from a commercially available human geenomic cDNA library in phage Lambda Fix (Stratagene). The sequence encodes a type I transmembrane protein with binding affinity for EPO. The gene and recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropolesis. It is believed that the EPO receptor is dysfunctional in individuals with Diamond Blackfan anaemia, and may be hyperactive in poly-
cythemia vera.
See also Q05747 (murine EPO receptor clone).
1883 BP; 320 A; 607 C; 584
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q05748
Q05748;
                                                                                                                                                                                                           P-PSDB; R06512.
                                                                                                                                                                                                                          D'andrea A, Wong G; WPI; 90-260931/34.
                                                                                                                                                                                                                                                    03-FEB-1989; US-306503.
(GENE-) GENETICS INST I
(WHIT-) WHITEHEAD INST.
                                                                                                                                                                                                                                                                                  01-FEB-1990;
03-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                             EPO receptor gene. Erythropoietin; Di
                                                                                                                                                                                                                                                                                                               09-AUG-1990.
                                                                                                                                                                                                                                                                                                                            WO9008822-A.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; cDNA; 1883 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPO receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 145..1759
                                                                                                                                                                                                                                                                                                                                                                                               Diamond Blackfan anaemia;
                                                                                                                                                                                                                                                                    INC.
                                                                                                                                                                                                                                                                                                                                                                                               polycythemia vera;
           <u>ი</u>
           372
                                                                                                                                                                                                                                                                                                                                                                                                88.
```

Residue Identity = Gaps = 50% 208 Conservative Substitutions 798 Mismatches

0

CG--TCAGGCGG--GCCCCACCCACCACAGCTGTCCCCAGCAGA----ACCTCTCTAGTCCTCACACTG---

GACCTCCCAGGGC--CTG--GTGGCAGTGTGGACATAGTGGCCATGATGAAGG-CT-CAGAAGC-ATCCT

GCT--GCC-TGCT--GTGGACTTTAGCTTGGGAGAATGG-AAAACCCAGATG----GAGGAGACCAAG-GC

AGAGCCTCCTTGGAACCCAGCTT--CCTCC-AC-AGGGCAGGACCACCAGCT-CACAAGGATCCCAT

CTCAGGAAGGGTAAGGTTCTCAGA----CACTGCCGACATCAGCAT--TGTCTCATGTACAGC--TCCCT-T

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AGAG-CGAGTTTGAAGGCCTCTTCACCACACCCACAAGGGTAACTTC-CAGCTGTGGCTGTACCAGAATGATGG

TICCCTGTG-GTGGAGCCCCTGCACCCCTTCACG-GAGGACCCACCTGCTTCCCTGGAAGTCCTCTCAGAG

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3

1690 PT infection, myelopoietic dysfunction, etc.

PS Example 3; Fig 2; 38pp; English.

CThis sequence was obtained by sequencing a cDNA subcloned into an M13 CC Inding vector. The cDNA was obtained by reverse transcribing poly A CC NNA obstained from a phorbol 12-myristate 13-acetate stimulated thuman monocytic cell line U937. This was packaged into a lambda gt10 CC library, which was screened with an appropriate murine cDNA probe.

CC clibrary, which was screened with an appropriate murine cDNA probe.

CC TO screen for human homologues of murine MIP-1alpha, a 236bp KpnI-CC murine MIP-1alpha mature coding sequence. For homologues of murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC which encodes all but the first two amino acids of mature murine CC then subjected to a second round of hybridisation, and it was not possible twas found that under the wash conditions used to was found that under the wash conditions used to murine MIP-lalpha US-08-223-263-2 (1-1795) Q23729 Sequence en 1470 TTAAGC TAAAAGGGATACACAGGACTGAAAAGGGAATCATTTTTCACTGTACATTATAAACCTTCAGAAGCTATTTTTT CTCAGGAGCAGGGGCATTGCTGTGTGTCTGCCCAA---TCCATCCTGCTCAGGAAACCACAA--CCTTG CAGTATTTTAAATA----TGTATAG---CCCTGCAGGGCGCCCCTGGGAGA---CAACTGGACAAGATTTCCTACTTTCTCCTGAAACCCAAAGCCCTGG ATCAGGGATCCAATATGACTCAGAGAACCAGTGCAGACTCAAGACTTATGGAACAGGGATGGCGAGGCCTCT 13-SEP-1991; U06489. 13-SEP-1990; US-582636. Sequence encodes human MIP-1beta Macrophage inducible protein; cancer myelopoietic dysfunction; autoimmune Expression of pure mammalian macrophage inducible proteins in yeast - to produce MIP for treatment and diagnosis of cancer, P-PSDB; R22712. Gallegos C A, Tekar WPI; 92-132088/16. /product= human_MIP-lbeta WO9205198-A. Homo sapiens. Q23729 standard; DNA; 582 Q23729; (CHIR-) CHIRON CORP.

Gallegos C A, Tekamp-Olson 22-SEP-1992 (first entry) 1700 1840 1340 Sequence encodes human 1780 1710 Location/Qualifiers 39..315 1350 1720 ₽₽ Þ 1850 ----TTTTTTTGCTGCAGA-GCTAGCTCTGCAG-CTCGAG
1850 1860 1870 1880 X cancer diagnosis;
oimmune disease; s 1360 MIP-1beta 1730 1800 1370 1740 1810 infection; 1380 1750 1820 1390

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18

Residue Initial 88888888 400 330 ATATTAGTTTAGCCAAAGGAT-AAGTGTCCTATGG--GGA--TGGTCCACTGTCACTGTTTCTCTGCTGTTG 490 500 510 520 530 540 550 480 490 500 510 520 530 540 GGAGCAG-TGACCTTCTGCTGGAGGAGGAGTGATGGCAGGAGGAACAACTGGGAACCAACTTGCCTCTCATC 00 410 420 430 440 450 460 470
TGCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGGACATT-CTG CACCGCGAG TCCCTTCTCTTAATTTAATCTT—TTTTATG—TCCCGTGTTAATTGTATTAGGTGTCA-TTTCCATTATTT 430 440 450 460 470 TGA-GCCCGGATGCTTCTCATGAGACACATCTCCT--CTCATA--CTCAGGACTCCTCTCCGCAGTTCCTG-TGACTCCCATGTCCTTC-ACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGC GCCAGC-CAGACA-CCCCGGCCA---GAATGGAGC-TGACTGAATTGCTCCTCGTG-GTCATGCTTCTCCTA 130 140 150 160 170 170 180 190 - AGTIGCAGAGAGGCCTAAAGAGGGCCCAAACAGGGAAGCCAC GCTGCCTTCTGCTCTC-CAGCGCTCTCAGCACCAATGGGCTCAGACCCTCCCACCGCCTGCTGCTTTTCTT/ and beta. Insert DNA was then subcloned into an M13 vector and sequenced. It was found human MIP-lalpha has 68.5% homology (740 nucleotide overlap) with murine MIP-lalpha, and 57.8% nucleotide homology (555 nt overlap) with murine MIP-lbeta. Human MIP-lbeta has 59% homology (559nt overlap) to murine MIP-lalpha and 72.7% homology (50nt overlap) to murine MIP-lbeta. See also Q23728, R22711, 2.
Sequence 582 BP; 129 A; 163 C; 120 G; 170 T; Score Identity 360 160 340 tt 11 11 370 210 132 48% 64 100 170 Conservative Substitutions Optimized Score = Matches = 380 110 390 120 230 190 241 290 400 130 Significance Mismatches 410 140 210 7.39 244 0 420



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CAAATACATGGATAACACATTTGA---
560
570
```

US-08-223-263-2 (1-1795) Q05297 Sequence en Q05297 standard; cDNA; 711 BP. Q05297; Sequence encoding Act-2 lymphokine/cytokine-like

27-NOV-1990 (first entry)
Sequence encoding Act-2 lymphokine/cytokine-like
Act-2; human lymphokine/cytokine-like protein; mi polyA_signal /*tag= b Homo sapiens. 27-NOV-1990 g) Location/Qualifiers 109..384 665..670 ke gene. mitogenic;

gs

ALD COCOCO PUT THE PROPERTY THE SECOND PROPERTY THE PROPE 28-JUN-1990.
15-DEC-1989; U05603.
16-DEC-1988; U5-285489.
(USDC) US SEC OF COMMERCE.
SIEBENLIST U, ZIPFEL PE, KELLEY K, IRVING WPI; 90-224535/29. P-PSDB; R05900. WO9007009-A. polyA_signal /*tag= c LEONARD WJ; 678..683 SG, NAPOLITANO

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New lymphokine-cytokine-like genes - isolated by subtraction cloning and hybridisation using mRNA from activated peripheral blood T cells. Disclosure; 137pp; English.

Probes raised to the gene product may be used in bloassay of the product, useful in detecting tumour cells, genetic defects in the inflammatory response, or in vivo, for the detection of immune system activation. The proteins may also be used to determine the presence of their receptors.

Sequence 711 BP; 172 A; 203 C; 139 G; 197 T;

Residue Initial Identity Score u II П 132 47% 64 Optimized Score = 261 Matches = 310 Conservative Substitutions Significance Mismatches 11 11

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I II II CACCGCGAG-230 130 140 150 160 170 180 190 AGTICCAAGAGACCCTAAACAGGGCCCCAAACAGGGAGCCAC GAAGCTTCCTCGCAACTTTGTGGTA-GATTACTATGAGA-CCAGCAGCCTCTGCTCCCA

620 X 640
CTTCCTCCACAGGGCAGGACCACAGCTCA TTAAAAAAAAAAAAAAAAAAAA 710

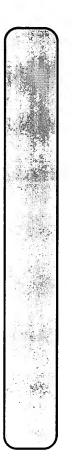
US-08-223-263-2 (1-1795) Q03682 Act-2 clone of gene encoding activated human

Q03682 standard; cDNA; 711 Q03682; ₽₽

SEEDIAC 12-SEP-1990 (first entry)

Act-2 clone of gene encoding activated human periferal blood mononuclear cell (PBMC).
Periferal blood mononuclear cell; PBMC; lymphokine; cytokine; mitogen; ds.

Homo sapiens.



Residue Identity Initial /*tag= a US7312001-A. 13-MAR-1990. The lymphokine/cytokine-like proteins are associated with the inflammatory response and/or have mitogenic activities. Antigens raised to the proteins may be useful in detection and purification, especially in bloassays of various tumour cells or genetic defects isolated using mRNA from activated mononuclear cells and T cells.
Disclosure; 84pp; English. H New lymphokine-cytokine genes P-PSDB; R04220. WPI; (USSH) US Dept Health & Human. Siebenlist U, Leonard WJ, Zipf 16-DEC-1988; 312001. 16-DEC-1988; US-312001. the inflammatory response. uence 711 BP; 172 A; 90-139708/18. 0 0 0 Location/Qualifiers 109..384 Optimized Score = 259.
Matches = 313
Conservative Substitutions Zipfel PJ, 204 Ç human Irving 138 periferal blood 259 . 313 <u>ი</u> SG, 197 Mismatches Kelly Significance ζ; 7.39 277

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610 620 X 640 CAGCTTCCTCCACAGGGCAGGACCACAGCTCA	550 CCTCC-TGGG 	480 GGAGCAG-TGAC ATATTAGTTTAC 560	400 410 TGCCTGCTGTG	430
20 ZACAGGGCAGG NAAAAAAAAAA) 710	560 GGCAGCTTTCT ATAACACATTT 640	490 CCCTTCTGCT IGCCAAAGGAT 570	420 GACTTTAGCT AATTTAATCT 510	440
X 640 SACCACAGCTCA 1 1 1	570 TIGGACAGGTCC TIGATTCTGTGT 650	500 GGAGGGAGTG C-AAGTGTCCT 580	430 TGGGAGAATG TTTTTATG	450
¥ 10	550 560 590 590 600 CCTCC-TGGGGCAGCTTTCTGACAGGTCCG-TCTCCTCCTTGGGGCCCT-GCACCCTTCGTAACCCTTCGTAACCCTTCAAAACCCTTAAAAATAAAATAAAATCCAGACAAATACACTGTAAAAATTAAAATTAAAATCCATAAAATAAAATCCAGA630 640 650 650 660 670	480 490 500 510 520 530 540 GGAGCAG-TGACCCTTCTGCTGGAGGGAGTGATGGCAGCAGGGGACCAACTGGGACCCACCTTCTCCTCATC	0 410 420 430 440 450 460 470 TGCCTGCTGCTGCGACTTTAGCTTGGGAGAATGGAAGAAAACCCAGATGGAGAGACAAGGGACAGGACATT-CTG	460
	590 TTGGGGCCCT-G NATAAAACTTTAA 670	520 GGGACAACTGG 	450 ATGGAGAGACC A A A A A A A A A A A A A A A A A A	470
	90 600 -GCAGAGCCTCC NAAATAAAATCC 680	530 GACCCACTTG ICACTGTTTCT 610	460 CCAAGGCACAGG 1 GGTGTCA-TTT	480
	0 CTTGGAACC CAGA	540 CCTCTCATC CTGCTGTTG 620	470 ACATT-CTG CCATTATTT 550	490

US-08-223-263-2 (1-1795) Q28806 DNA encoding placental protein

Q28806 standard; DNA; 820 ΒP

Q28806; 01-MAR-1993 (first entry)

DNA encoding placental protein 1. PP14; antibodies; interleukin-1;

114. -1; IL-1; proliferation; allergic

autoimmune; inflammatory; subunits; 88

Homo sapiens.

sig_peptide
/*tag= a mat_peptide Location/Qualifiers 46..99

AU9218068-A.

13-AUG-1992.
05-JUN-1992; 018068.
28-JUN-1991; US-720591.
(BOLT/) BOLTON A E.
(HYAL-) HYAL PHARM CORP.
(INTE-) INTERMUNE. LIFE S
BOLTON AE. DYIZEGN A;
WPI; 92-323118/40.

SCI

non-

P-PSDB, R27167.
Portain placental protein 14 or related cpds. or specific antibodies, for control of e.g. arthritis, leukaemia or HIV infections
Disclosure; Page 33; 41pp; English.
Disclosure; Page 33; 41pp; English.
The DNA sequence encodes placental protein 14 (PP14), which may consist of two of the specified submits, linked covalently or recovalently. PP14 can be isolated from human placenta or blood amniotic fluid, seminal plasma, cultured cells, decidual



Residue 888888888888888 810 260 GACTGGGAATCCAAGAAGTTCAAGATCAACTATACGGTGGCGAACGAG-GCCAC-GCTGCTCGATACTGA 330 340 350 360 370 380 390 GCTTCCAACACCTGCTCCGAGG-AAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGG CTCATCCCTCCTGGG-GCAGCTTTCTGGACAGGTCCGTCTCCTTCG---GGCCCTGCAGAGCCTCCTTG --TGGCGACA-CTG-----AAGGCCCCTCTGAGGGTCCACATGACCTCACTGTTGCCCACCCCGAGGACAAC sarcoidosis and allergic dermatitis, conditions which cause infertility. lymphoproliferative diseases, e.g. malignant non-Hodgkin's lymphoma. Hodgkin's disease or malignant histicoytosis, neoplastic disease, e.g. leukaemia or HIV infection. PP14 may also used in the treatment of early miscarriage. the DNA shown. The PP14 cpds. expressed by the DNA are inhibitors of IL-1 prodn. and thus immune cell proliferation and function so can be used to treat allergic, autoimmune and inflammatory conditions, esp. rheumatoid arthritis, asthma, graft vs. host disease, organ rejection; systemic lupus erythematosus, atopic allergy inflammatory bowel disease, multiple sclerosis, psoriasis, or endometrial cells or organs or recombinant cells transformed with Identity TCTGGA-TTGTTGGAGACAAACTTCACTGCCTC-AGCCAGAACTACTGGCTCTGGGCTTCTGA H 0 B 820 BP; 132 50% 110 760 Matches = 444 Conservative Substitutions Optimized Score = Matches = 560 770 570 263 C; 840 780 230 710 207 G; 368 444 850 Mismatches Significance 790 240 158 T; 860 250 11 870 be

CTACGACAATTTCCTGTGTCTCTGCCTACAGGACACCACCACCCCCATCCAGAGCATCATCTGCCAGTACC 400 410 450 460

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10. AC DT 1080 1090 1100 1110 1120 1130 1140
CAGCCT---GGATATTCTCCTTCCCCAACCCATC--CTCCTACTGGACAGTATACGCTCTTCC--CTCTTCC 940 950 960 970 980 990 1000 1010

AAATCCCCGGATACCT-GAACAGGATACACGAACTCTTGAATGGAACTCGTGGACCTCTTCCTGGACCCTCA 530 US-08-223-263-2 (1-1795) Q29260 Human calcium channel 1290 1300 X
TCAGACACTGCCGACATCAGCATTGTCCATGTACA /notes mencodes for coding region EP-507170-A. O3-MAR-1993 (first entry)
Human calcium channel 27980/2.
Plasmid pl247-5.1.2.1.1; Ca-flux assay;
Homo sapiens. 670 P-PSDB; R27640. Cloned human neuronal calcium (FARB) BAYER AG. Franz J, Rae P, Unt WPI; 92-333446/41. 23-MAR-1992; 104970. 04-APR-1991; DE-110785. Q29260 standard; DNA; 4919 Q29260; 680 1230 Unterbeck A, from amino Location/Qualifiers 2..4483 of. 1030 n amino acid Ca-channel 1170 690 1240 ₽₽ 1040 Weingaertner 700 1250 ç 1050 88 710 1260 1060 useful 1270 1070 1280 730

Residue Identity 260 270 280 CT-GC-AAGGCTAACG--CTGTCCAGCCGGCCTCCTGCTTGTGACCTCCGAGTCCTCAGTAAACTGCTT CGTTGTCTTTGCTCTTCTAGGAATGCAGTTATTTGGAGG----TCATTGTGCTCACCTTGTTTGGCA-ACTACACGCT-ACTGAAT--GTGTTCTTGGCTATCGCTGTGGATAAT CAA-GAGCCTAAG-CCGCCTCCAT-GGC-CCCAAGGAAGATTCAGGGGAAGAGCCCCAAAACAGGGAGCCACG CTCGCCAACGCCAGGAACTGACCA---AGGATGAACAGGAGGAAGA--1040 1050 1060 1070 CCAGCCAG-ACACCCCG---GCCAGAATGGA-GCTGACTGAATTGCTCCTCGTGGTCAT-GCTTCTCCTAA-TTCTCC--ACCCGGATAGATTCC--TCACCCTTGGCCCGCCTTTG--CCCCACCCTACTCTGCCCAGAAGTG Human neuroblastoma cell line, hippocampus, frontal and temporal cortex and visual cortex cDNA banks were screened with a probe containing carp skeletal muscle Ca-channel CDNA. The cDNA clone pl247-5.1.2.1.1 was sequenced and found to comprise the complete gene after Domain I. The sequence can be inserted into a eukaryotic expression vector for use in transforming suitable host cells. Cell lines producing human neuronal calcium channel proteins can be used for screening for Ca channel ligands (agonists or antagonists). See 229259-22275. calcium flux assays to screen for neurone-specific calcium channel ligands Claim 2; Page 10-21; 101pp; German. X 10 20 30 40 50
TCT-TCCTACCCAT-CTGCTCCCCAGAGGGCTGCCTGCTGCACCTTGGGTCCT-GGAGCCC n n 4919 BP; 47% 228 Optimized Score = Matches = Conservative Substitutions 1147 A; 1285 C; -CAGGT-TTAACTTTAATGATGGGACTCC 752 Significance = 908 Mismatches = tions = 1314 G; -AGAGGCCT--TCAACCAGAAA -GATGGA--GGAGACCAAGG--

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CAGGTCCCTGGACCAAATCCCCGGATACCTGAA--CAGGATACACGAACTCTTG--AATGGAACTCGTGGAC

---TTAAGGAGGÁCCAACÁGTCT-GATGGTGTC---1860 1870 1880 -CAGAGGCTCCGGGCTGG-CAGGAGGCCTTG

2460 GCAACAAAGTCCTGAGGTATTTTGACTATGTGTTTCACGGGCGAGTTCACCTTTGAGATGGTTATAAAGATGA 30 2470 2480 2490 2500 2510 2520 2530 1680 1690 1700 1710 1720 1730 1740 CTTCCAACGCCCCCATCCCCTTT-ACTATT-CTCAGTGGGACTCTGATTCCCATATTCTTA-ACAGAT-C TCAGCACCACCCAACCCGATCCGGAGGGCCTGCCACTACATCGTGAA--CCTGCGCTACTTTGAGATGTGCAT 2330 2340 2350 2360 2370 2380 2390 CACTGATTCTCTAC---ATGCTCTTTTTCTGTGATAACTCTGCAAAAGGCCTGGGCTGGCCTGGCAGTTGAA--CAGAGGGAGAGACTAACCTTGAGTCAGAAAAC-AGAGAAAGGGTAATTTCCTTTGCT-TCAAATTCAAGGC AGAAGAAGCAGAAGAAGGAGAAGCGTGAGA-CAGGCAAAGCCATGGT-GCCCCACAGC-TCAATGTTCATCT 1610 1620 15502200 1760 1630 1560 2280 1570 1640 2290 1780 1580 1650 2300 1790 1590 1660 1600 1670

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11. US-08-223-263-2 (1-1795) Q06470 Sequence en Sequence encoding complete form of human RF-X prot

Residue Identity Initial Purified proteins and compsns. - regulate expression of MHC class genes and bind to controlling DNA sequences.

Claim 11, Fig 9; 83pp; English.

The sequence encodes a protein which regulates the expression of MHC class II genes by binding to DNA sequences which control this expression. The protein causes down-regulation, useful for the prevention and treatment of autoimmune diseases such as Insulin Dependent diabetes, Multiple Scierosis, Lupus Erythematosis and Rheumatoid Arthriris. The protein can also be used for screening and identifying substances capable of inhibiting the expression of the MHC II genes. P-PSDB; R08338 18-APR-1990; E00625. 18-APR-1989; EP-106944. 14-AUG-1989; EP-115008. (MACH/) Mach B. /*tag= a WO9012812-A. Sequence encoding complete form MHC class II; down regulation; a Q06470 standard; DNA; 3086 Q06470; 25-FEB-1991 (first entry) See also Q06469 Sequence 3086 WPI; 90-348429/46. Mach B; 01-NOV-1990. Homo sapiens. Score H H ij and BP; Location/Qualifiers 94..3033 1 Q07000. ; 603 A; Optimized Score = 756 Matches = 914 Conservative Substitutions 쁑. autoimmune of human RF-X protein 1109 C; disease; 934 Mismatches <u>و</u> Significance 440

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140

150

160

180

CTCCATGGCCCCAGGAAGGATTCAGGGGAGAGGCCCCAAACAGGGAGCCA--CGCCA--GCCAGACACCCCG

160

170

180

190

CCCAG--CCGCCACA--GGCCCGCCACAAGCCGAGCCCAGCCACCACCACCCCCA

200

e de la

340

AG-CAG-TGACCCTTCTGCTGGAGGGAGTGATGGCAGCAGCGGGACAACTGGGACCAACTTGCCTCTCATC

480

490

500

510

520

| 820 | 840 | 850 | 860 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 | 870 610 620 630 640 650 660 670 CCAGCTTCCTC--CACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACAC 890 900 910 920
GGGATTCAGAGCCAAGATTCCTGGTCTG-CTGAACCAAACCTCCAG---510 -GGGCACCCAGCAGCGGCTGCT 520

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GGGCAGCAGCCGAGCACGGGCTGTCGGACATCAGCGCCCAGGT US-08-223-263-2 (1-1795) Q24676 Encodes par

Encodes partial MPLV-env

related

polypeptide.

Encodes partial MPIV-env related polypeptide. Myeloproliferative leukaemia virus; envelope protein; haematopoletic cell; Growth Factor receptor; ss. Q24676 standard; DNA; 552 BP. Q24676; Myeloproliferative leukaemia virus. 05-NOV-1992 (first entry) Location/Qualifiers gp70;

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Charon M, Gisselbrecht S, Penciolelli JF, Souyri
Tambourin P, Varlet P, Vigon I, Wendling F; 30-APR-1992. 19-OCT-1990; F00762. 19-OCT-1990; WO-F07623. /*tag= a W09207074-A.

Polypeptides similar to v-mlp protein of MPLV - treatment of myeloproliferative diseases Claim 10; Page 57-8; 75pp; French. P-PSDB; R27660. for diagnosis one

WPI;

92-167154/20.

This nucleotide sequence is one of 6 claimed sequences which code for polypeptides related to MPIV env protein. The proteins have on or more of the following properties: they are involved in the ligand-fixing or signal-transmitting function of haematopoletic growth factor receptors; they are recognised by antibodies to the protein with GENESEQ accession number R23970; when produced from the MPIV genome they can induce/promote proliferation of haematopoletic cells and/or are involved in differentiation of haematopoletic cells. The precise identity of sequence Q24675 is not further described in the specification.

See also R23971 and Q24674-7.

Sequence 552 BP; 106 A; 193 C; 135 G; 118 T;

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Initial Residue 70 X 80 90 100 110
CTCCACCGGATAGATTCCTCACCCTTGGCCGCCTTTGCCCCACCCTAC-TCTGC---CCAGAAGTGCAAG Score Identity 11 0 11 124 53% 94 Optimized Matches Conservative Substitutions Score 265 326 Significance Mismatches 11 11 9 5.86 191

CTAGA-GCTGCGCC---X 10

---CCCGAGCTCGCTACAGCTTGCAGCTGCCAG---GCTCAAC

13.

US-08-223-263-2 (1-1795)

Initial Residue 190 GAGCCT--AAGCCGCCTCCA----TGGCCCCAGGAAGGATTCAG---17-FEB-1994. 04-AUG-1993; J01095. 04-AUG-1992; JF-208077. 13-NOV-1992; JF-327619. 26-FEB-1993; JF-061431. (SAGA) SAGAMI CHEM RES CENTRE.

(SAGA) SAGAMI CHEM RES CENTRE.

(WAI) 94-065688/08.

P-PSDB; R46106.

P-PSDB; R46106.

CDNA of human origin and proteins coded by it - which may kexpressed by in vivo or in vitro translation using sense RN expressed by in vivo or in the cDNA.

Claim 1; Page 63-65; 167pp; Japanese.

Claim 1; Page 63-65; 167pp; Japanese.

MRNA expressed in human fibrosarcoma cell line HT-1080 was isolated and used to construct a cDNA library using vector. Homo sapiens. W09403599-A. Human cDNA; library; enzyme; protein; ss. 19-OCT-1994 (first entry)
Phenylethanolamine-N-Me-transferase like protein Q57445 standard; cDNA to mRNA; 792 BP. Q57445; pKA1. Clone HP00137 encoding Phenylethanolamine-N-Me-transferase like protein was isolated. Sequence 792 BP; 192 A; Identity Score 140 200 (I II II Phenylethanolamine-N-Me-transferase 124 51% 145 150 210 08 Optimized Score Matches Conservative Substitutions 150 220 160 90 207 C; **H** II 230 100 218 G; 352 447 170 like Mismatches 240 Significance 180 110 protein 180 RNA 250 120 R 5 190

60 70 80 90 100 110 120 CCTTCTCCACCGGATAGATTCCTCACC-CTTGGCCCGCCTTTGCCCCACCCTACCTCTGCCCAGAAGTGCAA ATGGAATCAGGCTTCACCTCCAAGGACACCTAT--CTAAGCC-ATTTTAACC--CTGGGGAT X 10 20 30 40 50 -CTCCTCTGTGTTGTGAATCCTTTAAGGAGATCGTC-GT-CACTGA 220 230 240 250 -GGGAGAGGCCCCAAACA----GGGA -TCCTCAGTAAACTGC 6.86 279

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710 TGATCTCGCAA--AGTTATTCTTCCACCATGGCCAACAACGAAGGACTTTTCTCCCCTGGTGGCGAGGA-AGC .0 720 730 740 750 760 760 730 740 750 760 770 780 7 CTGCGTCAGGGGCCCCACCACCACGAGGTCCCCAGCAGAACCTCTCTAGTC-CTCACA----AGAG-CCTCCTTGGAACCCAGCTTCCTCCACAGGG--CAGG-ACCACGC-TCACAAGGATCCCAATGCCAT CGAGCTCCCAAACAGGACTTC-TGGATTGTTGGAGACAA---CCCCCTGGGCCGGGAGGCAGTAGAGGCTGCTGT----GAAAGAGGCTGGCTACACAATCGAATGGTTTGAGG 650 650 670 680 690 700 CCAGACCTC---GGGGCC-CT--CCCCTTA-CCCCCGGCTGACTGCGTGCTCAGCACA---CTGTGT-CTGGATGCCG-CCTGC 870 X 089 880 820 480 830 -ACTTCACTGCCT--CAGCCAGAACTAC 490 840 -CCTTTGACI 850 790 -CTGA-A

- 14. US-08-223-263-2 (1-1795)
 Q24675 Encodes MPLV-env related polypeptide

- X E D A D Q24675 standard; DNA; 1307 BP. Q24675; Q246775; Q5-NOV-1992 (first entry) Encodes MTLV-env related polypeptide. Myeloproliferative leukaemia virus; envelope protein;



Residue Identity Initial PT Polyperbides similar to v-mlp protein of MPIV - for diagnosis and pri treatment of myeloproliferative diseases
PS Claim 10; Page 52-56; 7bpp; French.

This nucleotide sequence is one of 6 claimed sequences which code for polypeptides related to MPIV env protein. The proteins have one cor more of the following properties: they are involved in the cliqued fixing or signal-transmitting function of haematopoietic growth factor receptors; they are recognised by antibodies to the protein with GENESEQ accession number R23970; when produced from the MPIV genome they can induce/promote proliferation of haematopoietic cells and/or are involved in differentiation of haematopoietic cells. The precise identity of sequence Q24675 is not further described in the specification.

See also R23971 and Q24674-7.

See also R23971 and Q24674-7. (INRM) INSERM INST NAT SANTE & RECH MEDICALE. Charon M, Gisselbrecht S, Penciolelli JF, Souyri Tambourin P, Varlett P, Vigon I, Wendling F; WPI; 92-167154/20. /*tag= a W09207074-A. Myeloproliferative leukaemia virus. P-PSDB; R27659. 19-0CT-1990; F00762. 19-0CT-1990; WO-F07623. 30-APR-1992. haematopoietic cell; Growth Factor receptor; Score 0 0 ł 120 53% 134 Location/Qualifiers Optimized Score = 381 Matches = 471 Conservative Substitutions Mismatches Significance = Z 6.60 one 269 0

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330 340 350 360 370
G--ACTCCCAT---GTCCTTCACAGCAGACTGAGCCAGTGCC-CAGAGGTTCACCCTTTGCCTACACCT--G 830 TA-CTGC-CCAGAGCTCTGTCTCTGCAG 1290 1300 X 800 810 820
AACGAGCTCCCAAACAGGACTTCTGGATTG CTGGGCCTACTGCTG-CTAAAGTGGCAATTTCCTGC-770 780 790 800 GT-TGCCA-----CCCCACTCCCCCTCTGGCTTTATAACACTGATCACTC-CAAGATGGCTGCTCACAAAT 1230 1240 1250 1260 1270 1280 730 740 750 760 770 780 790 CTGCGTCAGGGGGCCCCAC-CCACCAGC-AGCTGCCCCAGCAGAAC-CTCTCTAG-----TCCTCACACTG CATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGTCCACCCT ACCTTGCCTGCGGACCATGCC-CCTG-----TCTGTGTGTCCA--CCCATGGCTGAGACGGGGTCCTGCTGC 400 410 420 430 440 450 460 TCCTGCT--GCCTGCTGCACTTTAGCTTGGAAGAAAACCCAG-ATGGAGAGACCAAGGCACAG GGCCCTCGCTTCCAGACCTACACCGGGTCCTAGGCCAGTACCTCAGAG--ACAC----TGC--AGCCCTAAG ---CTTGCCT----CTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCCTCCTCCTTGGGGCCCTGCAG-1050 920 860 690 930 560 GCACTACAGGAG-ACTGAGGCA--TGCTTTGT 700 1070 940 810 1080 950 -AATCCTCCC 890

ID 040341 standard; cDNA to mENA; 6314 BP.
AC Q40341;
DT 09-AUG-1993 (first entry)
DE Sequence of a cDNA clone contg. the ADMLX gene associated

with

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15. US-08-223-263-2 (1-1795)

Q40341

Sequence of a cDNA clone contg. the

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X-linked Kallmann syndrome; ADMLX gene; diagnosis; PCR;

linked Kallmann Syndrome (KS).

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Nucleic acid sequence of gene with X-linked Kalimann syndrome - useful for diagnosing Kalimann syndrome by amplification to	SDB; R34445.	134456/16	Detit C:	I Legonis B Levillier	INVI CAUTEOR.	/TWCT TWCT D: CMTCH	_	15-100-1003	W09307267-A	0 = 0	/label= 13	q= n		/label= 12	q= m	/label= 11	Q= 1		= 10	g= k	exon 15051599	9	.	80	g= i	exon 12131357	= 7	-	exon 10071212	6		/label= 5	g= f		/label= 4	 469	/	Z = TB	/*tag= c		= 1	6	aq≔ a	CDS 1512193	o sapiens.	- :

Residue Identity = Gars = 1270 130 210 220 230 240 250 270
ACACCCCGGCCAGAATGGAGCTGACTGGATTTGCTC-CTCGTGGTC-ATGCT-TCTCCTAACTGCAAGGCTAA 60 70 110 110 120 CTTCTCCACCCGGATAGATTCCTCACCCTTGCCCCCCCCTTTGCCCCACCCTACTCTG-CCCAGAAGTGCAAG TITCCTGAAGCGTGTGCCCACAACAGGAACAACCGGATCAGAGGCATCATCTGGGATGACCCACGAAAATTAC ACTCCCTTTTC--AAAGACGACGACCCACTCGCCGCTGGAAGTCGGAAGCTCCCTTCTATCAGGATGGCCAA 1410 1450 1460 1470 AGCCTAAGGCGCCTCCATGGCCCCAGGAAGGATTCAGGGGAGAGGCCCCAAACAGGGAGCCAGGCCAG --TCCTTCACAG----detect genetic anomalies Claim 1; Fig 6; 60pp; French.

The nucleic acid sequence is derived from the ADMLX gene associated with KS (or Hypogonadotrophic hypogonadism and anosmia).

Oligonucleotide pairs which act as primers for specific amplification of the gene are used in amplification methods to detect genetic anomalies which cause KS. The primer pairs corresp. to the coding and non-coding regions of exon 1 of the ADMLX gene and one pair each for the other 13 exons.

Sequence 6314 BP; 1884 A; 1274 C; 1246 G; 1910 T; 1340 Score 1210 X 1550 1350 1220 290 120 47% 251 1490 1560 1360 Optimized Score = 751 Matches = 922 Conservative Substitutions 1230 360 300 1500 1570 1370 370 310 1580 1510 751 Significance 922 Mismatches 1250 1380 180 320 Significance = 15901520 380 1260 1390 330 1600 1530 6.60 748 0 1400



AGGACATTC--TGGGAGCAG-TG-ACCCTT--CTGCTGGAGGGAGTGATGGCAGCACGGGGACAACTGGGAC

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AGGACTGAA-AAGGGAATCATTTTTCACTGTACATTATAAACCTTCAGAAGCT---ATTTTTTTAAGCTATC

TGAGCT-TCCAACACC-TGCTC--CGAGGAAAGG--TGCGTTTCCTGATGCTT-GTAGGAGG-GTCCACCCT

AAAGGAGAGTAACAAATACACAA----TTCACACATAACACT-AAGCGTAAATCTAATCAATAAAATATATTT

CTAAGATCATTITTATCCTAGGTGATTTTTAAATGAAAATGTGTAATCT--AAAATATATACCAGCGAATTTAA

IntelliGenetics

Release 5.4

FastDB - Fast Pairwise Comparison of Sequences

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Listing for Mary Hale

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                                                                                                                                                                                      Query sequence being compared:US-08-223-263-2 (1-1795) Number of sequences searched: 358124 Number of scores above cutoff: 4841
                                                                                                                                                                                                                                                                                                                                                                                                         1000000-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Results file sq2.res made by
                                                                                                                     1000-
                                                                                                                                                                                                                                                                                                                                                                                                                         Results of the initial comparison of US-08-223-263-2 (1-1795) with: Data bank: EMBL-NEW 2, all entries
Data bank: GenBank 87, all entries
Data bank: GenBank-NEW 2, all entries
Data bank: UEMBL 41_87, all entries
100-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Tue 11 Apr 95 10:59:11-PDT.
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PARAMETERS

y K-tuple 1 Joining penalty 30 0 Window size 32 5 5 6 Alignments to save 15 0 Display context 10 SEARCH STATISTICS Median Standard Deviation 33 13.50 Total Elapsed 01:26:08.00 307267536 358124 4841	Cut-off raised to 26. Cut-off raised to 30. Cut-off raised to 33. Cut-off raised to 37. Cut-off raised to 42. Cut-off raised to 44. Cut-off raised to 47. Cut-off raised to 49. Cut-off raised to 52. Cut-off raised to 58. Cut-off raised to 58. Cut-off raised to 60. Cut-off raised to 60. Cut-off raised to 60. Cut-off raised to 60.	Number of residues: Number of sequences searched: Number of scores above cutoff:	Times: CPU 01:25:58.06	Scores: Mean 33		Initial scores to save 45 Optimized scores to save 0	Similarity matrix Unitary Mismatch penalty 1.00 Gap penalty 0.33 Cutoff score 5 Randomization group 0
alty to save text text Standard 13.50 Total El 01:26:08			.06	Median 33	SEARCH STATISTIC		
			Total Elapsed 01:26:08.00	Standard Devi	S	to save ntext	nalty e



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Page 43

Cut-off raised to 65. Cut-off raised to 68. Cut-off raised to 71.

The scores below are sorted by initial score. Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

1. HUMMICMPI 2. HSMICMPI	Sequence Name
Human c-mpl ligand (ML) mRNA, 1795 1795 1795 130.53 0 Human c-mpl ligand (ML) mRNA, 1795 1795 1795 130.53 0	Description
ligand ligand	
(ML)	
mRNA,	
1795 1795	Init. Opt. Length Score Score
1795 1795	Init. Score
1795 1795	Opt. Score
1795 1795 1795 130.53 1795 1795 1795 130.53	Sig. Frame
00	Frame

The list of other best scores is:

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mat_pe BASE COUNT	sig_pe CDS	TITLE TOURNAL MEDLINE COMMENT FEATURES SOURCE	1. US-08-223- HUMMICMPL LOCUS DEFINITION ACCESSION KEYWORDS SOURCE ORGANISM	34. CCT64CLU 35. HSCL3S2 36. MUSI9R 37. HUMMENIA 38. CHKBA3A1 39. HSPAIV 40. HSVWFAB 41. ADRCOMPGEN 42. HUMCYTNEWB 43. HSCYTNEWB 44. HUMGPIIB 45. HSGPIIB
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Substitutions

Score Identity . . . 1795 100% 0 Optimized Sco Matches Conservative Score 11 11 1795 1795 Significance Mismatches 130

Initial Residue Gaps

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US-08-223-263-2 (1: HSMLCMPL Human (1-1795) man c-mpl ligand (ML) mRNA,

complete

HSMLCMPL standard; RNA; PRI; 1795 ₽₽

05-JUL-1994 18-JAN-1995 (Rel: 42,

Created) Last upd updated, Version 2

Human c-mpl ligand (ML) complete

c-mpl ligand

Homo sapiens (human) Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; Vertebrata; Catarrhini; Mammalia; Hominidae.

de Sauvage F.J., Hass P.E., Spencer Gurney A.L., Spencer S.A., Darbonne Kuang W.J., Oles K.J., Hultgren B., S.D., Malloy B.E., W.C., Henzel W.J., Wong Solberg L.A.Jr., Goeddel

1 S.C.,

> "Stimulation of megakaryocytopoiesis c-Mpl ligand [see comments]";
> Nature 369:533-538(1994). mat_peptide CDS sig_peptide source **1**10 506826 /codon_start=1
> /product="c-mp1
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> /note="erythropoietin
> 506827" Location/Qualifiers ligand ligand" and homology mRNA. thrombopoiesis domain ď β 66..522; NCBI

Initial Score Residue Identity

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1795 100% 0

Optimized Matches

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Significance Mismatches

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Page 51

US-08-223-263-2 HSU11025 1740 Human (1-1795)megakaryocyte 1750 1760 growth 1770 and development 1780 factor 1790 ×

1730

KEYWORDS ACCESSION DEFINITION Uli025 Human HSU11025 megakaryocyte growth and development factor (MGDF) mRNA, 1341 bp 15-OCT-1994

ORGANISM group; Myperchondria; Eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostsichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalla; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. human.

SOURCE

AUTHORS Chang, M.S., Samal, B., Nichol, J.I., Swift, S., et, al. Identification and cloning of a megakaryocyte growth and development factor that is a ligand for the cytokine receptor Cell 77 (7), 1117-1124 (1994) Martin, F

TITLE

JOURNAL MEDLINE Samal,B.B. (bases 1 to 1341)

REFERENCE AUTHORS TITLE COMMENT JOURNAL Amgen NCBI Submitted (18-JUN-1994) Babru B. Samal, Developmental Biology, Amgen Inc., Amgen Center, Thousand Oaks, CA 91320, USA Direct Submission gi: Inc., Amgen Center, gi: 511223

FEATURES SGS /organism="Homo sapiens"
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BASE CO COUNT mat_peptide 298 ø /product="megakaryocyte growth and development
 452 c 294 g 297 t

Residue Initial Score Identity 0 H H 1338 0 Optimized Matches Conservative Score Substitutions 11 11 1338 1338 Significance Mismatches н 96.

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Page 52

250 260 310
GTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCCGCGCTCCTCCTGCTTGTGACCTCCGAGTCCTC
GTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTC
GTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTGACCTCCGAGTCCTC 540 550 580 580 590 FOR THE PROPERTY OF THE PR 210 390 140 360 400 220 150 90 370 300 230 410 160 90 380 310 240 420 170 100 390 320 430 250 180 110 400 330 260 440 190 410 200 130 420

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> Page 53

4. US-08-223-263-2 (1-1795)

HUMTA Human gene for thrombopoietin.

LOCUS DEFINITION ACCESSION Human gene for thrombopoietin. D32046

PRI

23-NOV-1994

thrombopoietin.

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/ JOURNAL MEDLINE BASE COUNT ORIGIN FEATURES COMMENT REFERENCE SOURCE TITLE AUTHORS ORGANISM exon exon exon CDS exon exon exon source Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae 1 (bases 1 to 7666) NCBI gi: Pharmaceutical Reseach Laboratory Kirin Brewery Co., Ltd. 95010765 thrombopoietin gene FEBS Lett. 353, 57-61 (1994) and Miyazaki,H. Sohma, Y., Akahori, H., Seki, N., Homo sapiens Homo sapiens blood DNA, clone lambdaHGT1 Phone: Japan Gunma Maebashi Kirin Brewery Co., Ltd.
2-2 Souja-machi 1 chome Yoshiaki Soma Submitted (08-Jul-1994) to DDBJ by: Molecular cloning and chromosomal localization of the human 1897 371 0272-54-8618 0272-52-2307. ø /number=5
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Initial Residue

Score Identity

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Optimized :

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1441 Significance 1504 Mismatches

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Conservative Substitutions

AACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTC----CTTGTGACCTCCGAGTCCTCAGTAAACTGC GGG-ACCCACTTGCCTCTCATCCCTCCTGGGGCA---GCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCC -TGCAAGAGCCTAAGCCGCCTCC-ATGGC-CCCAGGAAGGATTCAGGGGAGAGGCCC----CAAACAGGGAGC -GCTGGAGGG--AGTGATG-GCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGC -AGATCIGGC-CCIGGIGIIIGGCC

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7080 CTCATGTACAGCTCCCTTCCCTGCAGGGGGCCCCTGGGAGACAACTTGGACAAGATTTCCTACTTTCTCCTGA

5. US-08-223-263-2 (1-1795) HUMTHROMA Human thrombopoietin gene, complete cds.

DEFINITION Human thrombopoietin HUMTHROMA 6163 bp ds-DNA gene, complete cds.

29-JAN-1995

Locus

ACCESSION KEYWORDS SOURCE thrombopoietin. L36051

ORGANISM Homo sapiens Homo sapiens DNA.

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 (bases 1 to 6163)

Foster,D.C., Sprecher,C.A., Grant,F.J., Kramer,J.M., Kuijper,J.L., Holly,R.D., Whitmore,T.E., Heipel,M.D., Bell,L.A.N., Ching,A.F., McGrane,V., Hart,C., O'Hara,P.J. and Lok,S.

Human thrombopoietin: gene structure, cDNA sequence, expression, and chromosomal location

Proc. Natl. Acad. Sci. U.S.A. 91, 13023-13027 (1994)

REFERENCE AUTHORS

TITLE JOURNAL

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Residue Identity JOURNAL COMMENT FEATURES Initial BASE CO REFERENCE AUTHORS KEYWORDS SOURCE DEFINITION ACCESSION US-08-223-263-2 HUMTHROMB Hur 6040 ORGANISM 210 X 220 230 240 250 260 270 CCCGGCCAGAATGGAGGCTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTC source CDS Score Proc Homo 6050 Homo sapiens Foster, D.C., Sprecher, C.A., Grant, F.J., Kramer, J.M., Holly, R.D., Whitmore, T.E., Heipel, M.D., Bell, L.A.N., McGrane, V., Hart, C., O'Hara, P.J. and Lok, S. Human thrombopoietin: gene structure, cDNA sequence, Eukaryota; Animalia; Eutheria; Primates; I 1 (bases 1 to 1062) thrombopoietin and chromosomal location L36052 Human 11 11 11 223 <u>t</u> sapiens cDNA to thrombopoietin (1-1795)Natl. Acad. Sci. 1062 100% 0 ρ /product="thrombopoietin"
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GTSDTGSLPPNLQFGYSPSSPTHPPTGQYTLFPLPFTLPTVQLHPLLPDPSAPTFTP
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a 375 c 236 g 228 t thrombopoietin mRNA, 533216 1..10621..1062Location/Qualifiers 6060 /codon start=1 /note="putative; NCBI /organism="Homo sapiens"
/sequenced_mol="cDNA to mRNA" Optimized Score = 1062 Matches = 1062 Conservative Substitutions Haplorhini; 6070 mRNA, Chordata; mRNA. ss-mRNA U.S.A. 91, complete 6080 complete Vertebrata; Mammalia; ; Catarrhini; Hominida; gi: 533217" 13023-13027 cds. cds. 6090 Significance Mismatches Hominidae (1994)6100 Kuijper, J.L., Ching, A.F., Theria; 0 0 0 76 003

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US-08-223-263-2 (1-1795) MUSTHROA Mus musculu

Locus

Mus musculus thrombopoietin mRNA, complete cds.

ACCESSION KEYWORDS DEFINITION Mus musculus thrombopoietin mRNA, L34169 MUSTHROA 1486 bp ss-mRNA complete cds

thrombopoietin

Mus musculus cDNA Mus musculus ç mRNA.

SOURCE

ORGANISM

Eukaryota; Animalia; Chordata; Eutheria; Rodentia; Myomorpha; Vertebrata; Mammalia; Theria;

(bases 1 to 1486) Muridae; Murinae.

JOURNAL MEDLINE COMMENT REFERENCE AUTHORS Iok, S., Kaushansky, K., Holly, R.D., Kuijper, J.L., Lofton-Day, C.E., Oort, P.J., Grant, F.J., Heipel, M.D., Burkhead, S.K., Kramer, J.M., Bell, L.A.N., Sprecher, C.A., Blumberg, H., Johnson, R., Prunkard, D., Ching, A.F. T., Mathewes, S.L., Bailey, M.C., Forstrom, J.W., Buddle, M.M., Osborne, S.G., Evans, S.J., Sheppard, P.O., Pressnell, S.R., O'Hara, P.J., Hagen, F.S., Roth, G.J. and Foster, D.C. Cloning and expression of murine thrombopoietin cDNA and stimulation of platelet production in vivo

TITLE

508540 1..1486 Location/Qualifiers

FEATURES

source

CDS

/organism="Mus musculus" /sequenced mol="cDNA to mRNA" 174..1244

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BASE COUNT ORIGIN 331 /product="thrombopoietin"
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Residue Initial Identity Score 0 0 0 694 77% 83 Optimized Matches Conservative Score Substitutions 11 15 1155 1198 Significance Mismatches a 11 B 48 8.97 258 0

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	1190 1200 1210 1210 1210 1210 1210 1210	1100 1110 1120 1130 1140 1150 1160 TTCCCCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCAC	1030 1040 1050 1060 1070 1080 1090 AGCCCGGACATTTCCTCAGGAACATCAGACAAGGCTCCCTGCCAACCCTCCAGCCTGGATATTCTCC	960 970 980 990 1000 1010 1020 CCTGAACAGGATACACGAACTCTTGAATGGAACTCTTGGAACTCTTTCCTGGACCCTCACGCAGGACCCTAGG	890 900 910 920 930 940 950 GGGATTCAGAGCCAAACCACACCACACCACACCACACCA	820 830 840 850 860. 870 880 TTCTGGATTGTTGGAGACATCTCACTGCCTCAGCCAGAACTACTGCCTCTGGGCTTCTGAAGTGCAAGCA	740 750 760 770 780 790 800 810 GGCCCACCACACACCTGTCCCCAGCAGAACCTCTCTAGTCCTCAAACAGGACCCCAAACAAGACACCACCACACACA	670 680 690 700 710 720 730 CTTCCAACACCTGCTCCGAGAAAGCTGCGTCTCCTGATGCTTCTGAGAGGTCACCCTCTGCGTCAGGCG	600 610 620 630 650 650 CCTCCTGGAACCCCAACGGGACCACACCCCAACGGACCCAACGATCCCAATGCCAATCTCCTCAG [530 540 550 560 570 580 590 ACCCACTTGCCTCCTATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCCTCCTCCTTGGGGCCCTCCAGAG	
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1340 1360 1370

8. US-08-223-263-2 (1-1795) HSTNSCN Human mRNA LOCUS DEFINITION ACCESSION KEYWORDS COMMENT REFERENCE REFERENCE SOURCE AUTHORS TITLE JOURNAL JOURNAL MEDLINE TITLE AUTHORS ORGANISM Zardi, L.

Direct Submission

Submitted (10-OCT-1990) to the EMBL/GenBank/DDBJ databases. L.

Submitted (10-OCT-1990) to the EMBL/GenBank/DDBJ databases. L.

Submitted (10-OCT-1990) to the EMBL/GenBank/DDBJ databases. L.

Zardi, ISTITUTO NAZIONALE PER LA RICERCA SUL, CANCRO VIALE BENETTO XV. 10, 16132 GENOVA, ITALY

2 (bases 1 to 7280) carnemolla, B., Saginati, M., Leprini, A., Casari, G., This sequence conflicts with M24630 (Gulcher J.R. P.N.A.S. $86:1588-1592\,(1989)$. Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; (bases 1 to 7280) extracellular matrix protein; Human mRNA for tenascin. 91187670 Nucleic Acids Res. 19 (3), 525-531 (1991) antibodies Human tenascin: primary structure, pre-mRNA splicing patterns localization of the epitopes recognized by two monoclonal Homo sapiens human. X56160 HSTNSCN Human mRNA for tenascin. 7286 bp RNA tenascin. Vertebrata; Mammalia; Catarrhini; Hominidae. 01-SEP-1992



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FEATURES CDS CDS source repeat_region repeat_region NCBI V.3.50 gi: TTRILDAPSQLEVKOVTDTTALITWFKPILEIDGIEITYGIKDVFGDRTTIDLITEDENQ
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-CTGCAAGGAGCA-AAGATGTCCCAGT 1730 1740

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Residue Identity Initial Score BASE COUNT ORIGIN 270 280 290 310 320
-GGCTRACGCTGTCCAGC—CCGGCTCCTCGTGTGTGCTCTCGAGT—CCTCAGTAA—CGCTAACGTAA—CGCTCAGTAA—CAGGGCTCTCCTGCTTGTG-GACGACCAGTGCGTCTGCGTCTTCACC
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1560 1570 1580 1590 1600 1610 1620 60 70 80 90 100 110 120
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1630 1640 1650

US-08-223-263-2 (1-1795) HUMHXB Homo sapien Homo sapiens hexabrachion mRNA, complete cds

LOCUS
DEFINITION
ACCESSION
KEYWORDS HUMHXB 7390 bp ss-mRNA PRI Homo sapiens hexabrachion mRNA, complete cds. M55618 hexabrachion; tenascin 08-NOV-1994

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QRKLELIGLITGIĞYEVMÜLMLIPRASNE SWYADEGYEDNEVLKIBDTKKQSEPLE; RRQTUSAI LATTAMGSERÜ IF SDITAK RRAQPATAMQBATATUDSYU IS YITAK VIVDGTKYQTRLYKLI FÖVEYLVS I IAM SEALARWQPATATUDSYU IS YTGEKVPE; KGPQKSSTITAKFTTDLDS PROLITATEV KENLYGEDTTSGLYTI YLMGDKAQALEVFQI AGFGDREEF LHWLGLDNINKITAQGQYI KKYEGYSCTAGDSYAYINGRSP STFDKD; GDNNHSQGVNWFHWKGHEHS IQFADMKLI GDNNHSQGVNWFHWKGHEHS IQFADMKLI	TAXABLE TO THE TAX	/number=13	/ (1010)	$4169\overline{4}441$	/codon start=1	/number=12	/ yeare- nan	\(\cappa_0\) \(\ca	1168	/codon start=1	/number=11	/gene="Hxb"	36233893	υI .	/codon start=1	/number=10	/gene= mxp			/codon start=1	/number=9	Actic Try			/codon start=1	/number=8	/gene="Hxb"	2990	7	(codon at art = 1	/number=7	/gene="Hxb"	28102995	/codon_start=1		/gene="hxp"	\\ \lambda \lambda \lorent \cdot \cd	פומדר	/codon start=1	/number=5	/gene="Hxb"	23832539	/codon_start=1	/number=4	'gerle="hxp"	\(\(\chi\)\(\c	33C3 33C3	Codon of art = 1	/number=3	/gene="Hxb"	20032266	/codon_start=1	/number=2	/gene="Hxb"	3932002	SNE KNILEGAKAKA"	ON THE TRANSPORT OF THE PROPERTY OF THE PROPER	DE LEAD VELLE PER BOOK DE LE CONTROL DE LE CONTROL DE L'AUTOUR DE	CONCERNING AND MANAGEMENT AND	TSDGGGWIVFLRRKNGRENFYONWKAYAAGFGDRREEFLHWLGLDNLNKITAOGOYEL	NGPLRSNMIQTIFTTIGLLYPFPKDCSQAMLNGDTTSGLYTIYLNGDKAQALEVFCDM	ETALLTWRPPRASVTGYLLVYESVDGTVKEVIVGPDTTSYSLADLSPSTHYTAKIOAL	RTVSGNTVEYALTDLEPATEYTLRIFAEKGPQKSSTITAKFTTDLDSPRDLTATEVQS	FEESEPVSGSFTTALDGPSGLVTANLTDSEALARWQPALATVDSYVLSYTGEKVPELT	HELD STORY TO A THE STORY OF TH	JONNY I DAN TAOMINEN DE LA CONTRACTOR DE L LOS MAIS LA CONTRACTOR DE	LAPERTRILITALREATEVELETACIONESOTVOA LATTAMGSPKEVLESDITEN	LRAE IVTEAEPEVDNLLVSDATPDGFRLSWTADEGVFDNFVLK I RDTKKOSEPLE I TL	ENAFDSF LVTVVDSGKLLDPQEFTLSGTQRKLELRGLITGIGYEVMVLWLHPRASNKP	I SGLEPSTOFI VILEGLAPSIRTRIL SATATTEALPLLENLTISDIN PYGFTVSWMAS	
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	540 CCTCTCAT GCCAG	470 CTGGGAG CATGG-C	410 TGCTGT0 TGGGCAGT	340 CCCATGT GCCCTG- 1710	270 CTAACGC' CCCAGGG	200 AGCCAGA AGCCAGA A I I CG-CTGT	30 GAGCCTAAG † † 1510	60 CCTTCTCI AGGACTGI	CCAATG	Score Identi
610	O TCCCTCC GCACTCC 910	480 CAGTGACCO CAGGGCCGO	410 GTGGACTT 	CCTTCAC 	280 TGTCCAGC ACTGCAGC 1650	210 CACCCCGG 	140 AGCCGCC AGGCT	70 CACCCGG CAGCCAG	X TCTTC-C GCTGCAG 1370	ty =
200	550 TGGGGCP TGCCCCP 1920	CCTTCTC	420 TAGCTTG- TGCCATGP	350 AGCAGAC AGAACTC	CCCGG CAACAGG	0 GCCAGAAT GCATGTGT 1590	150 TCCATGGO TCAAGGG- 1520	70 80 CCCGGATA-GATTCCTCA	10 TACCCAT TGGCCAT 1380	180 C 49* K 226 C
	540 550 560 570 580 590 590 590 590 590 590 590 590 590 59	470 480 500 510 520 ATCTGGAGGAGGAGGAGGAGGAGGAGCAAGTGGAAGGAGGAGCAAGTGATGGAAGGAGGAGGAGGAGGAGCAAGTGATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	410 420 430 440 450 460 460 460 460 460 460 460 460 460 46	340 350 360 370 380 390 400 ACTCCCARGICCTCACACCAGACTGACCAGTGCCCACAGGTTCACCCTTTGCCTACACCTGTC-CTC-CTC 1 1 1 1 1 1 1 1 1	270 280 290 310 320 320 330 320 330 330 330 330 330 33	200 210 220 250 260 260 260 260 260 260 260 260 260 26	130 140 150 160 170 180 190 CAAGAGCCTAAGCCCCCCATGGCCCCAGGA-AGGATTCAGGGGAGAGGCCCCAAACAGGGAGCCAC	60 70 100 110 120 AGCCCTTCTCCACCGGATA-GATTCCTCACCCTTGGCCCGCCTTTGCCCCACCCTACTCTGCCCAGAAGTG	X 10 20 30 40 50 TCTTC-CTACCCATCTGCT-CCCCAGAGGGCTGCCTGCTGTGCACTTGGGTCCTGG	Optimized Score = 781 Matches = 943 Conservative Substitutions
05.9	G-GACAG GCAACAA	500 GAGTG-ATG GCCAGTGCAT- 1870	430 AATG-GA TATGGGC 1800	3 GTGCCCA -TGTCCA 730	30 TGCTTGT TGTGTG- 1670	230 GACTGAA' GA-TG-A' 1600	160 A-AGGAT ACTGCAG 1530	90 ACCCTTGGC NATGACTGT	20 -CCCCAG GTGTCAA 390	d Score
640	570 GTCCG H CTTAGGA	-ATGGCA CATCT	430 440 450 450 450 450 450 450 45	370 :AGAGGTTC 	0 GACCTCC GACGGAC	TTGCTCC CGGCTAC	170 TCAGGGGA(TGACATGA(1540	CCGCCTT CACAGTC 1470	30 AGGGCTG TGGGCAG 1400	= = bstitut
n	-TCTCCT } CAATGCG	510 CAG-CACGGGAC 	0 G-ATGGA GCAAGGA B10	380 ACCCTTT TGCCATG	310 GAGT-CC -AGTGCG 680	240 CCTCGTGGT ACACAGGGG	0 AGAGGCC AGCTGCC	100 TTGCCCCACCC CGGGGCCGCTC	CCTGCTG TGTG-TG	
א א	580 CCTTGGG TCTCGGG	GGACA GGGCTTC	450 GGAGACC GCA-AAG 1820	39 GCCTACA GCC	TCAGTAA-	250 CATGCTT AAGACTG 1620	180 CCAAA CCAATGA 1550	110 CCCTACT CTGTGTC	40 TGCACTT TGTGATG	Significance = Mismatches = =
660	590 GCCCTGC CCGCTGC	520 AACTGGGA CACAGGCC 1890	460 AAGGCACA ATGTCCCA 18	CCTGTC-	320 ACTGCTTC GGACGGCTTC 1700	26 CTCCTAACT CCGGGATC	CAGGGAGO	12 CTGCCCA GAGGGCA 1490	GGG AGGGCTA 1420	
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TCCTTGGAACCCAGCTTCCTCCACAGGGCAG-GACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGC

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GACAC-TGCC---

10. US-08-223-263-2 (1-1795) HSHXB Homo sapiens hexabrachion mRNA, complete cds.

XXXXXXXXX HSHXB standard; RNA; PRI; 7390 BP

M55618;

21-FEB-1991 17-DEC-1994 (Rel. 27, Created)
(Rel. 42, Last updated, Version 3)

Homo sapiens hexabrachion mRNA, complete cds.

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Page 7

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1-7390
Nies D.E., Hemesath T.J., Kim J.H., Gulcher J.R., Stefansson K.;
"The complete cDNA sequence of human hexabrachion (Tenascin). A multidomain protein containing unique epidermal growth factor repeats";
J. Biol. Chem. 266:2818-2823(1991). exon exon exon exon NCBI Gulcher J.R., Nies D.E., Alexakos M.J., Ravikant N.A., Sturgill M.E., Marton L.S., Stefansson K.; "Structure of the human hexabrachion (tenascin) gene"; Proc. Natl. Acad. Sci. U.S.A. 88:9438-9442(1991). Homo sapiens (human) Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; CDS Key [2] 1-7390 exon exon source hexabrachion; tenascin. gi: 184483 /partial
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593..2002
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Listing for Mary Hale

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/codon_start=1	ijĘ	f	a t	/gene= nxb	. (n	codon	/number=19	gene="	7	/codon start=1	er	≡ " Hx	5527	/codon start=1	/number=17	1 3	2383	/codon start=1	T=16	١ •	ᆑ	CT=T	/gene="Hxb"	7	/codon start=1	er	11 :	4714	5+54+1	/gene="Hxb"	441	codon	er.	/qene="Hxb"	38964168	1	/gene="hxp"	36233895	/codon_start=1	н	ene="Hx	3622	/number=9	/gene="Hxb"	.3349	/codon start=1	/number=8	308	st	number	/gene="Hxh"	910 300
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Listing for Mary Hale

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				exon				exon				exon				exon				exon				exon
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100

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1590 1600 1610

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Page 8

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CAGCATCACCCTGGAATGGAGGAATGGCAAGGCAAGCTATTGACAGTTACAG-AATTAAGTATGCCCCCAT-C CAGCAATACTCATCAGAGCAGCTAGCTCTTTG-GTCTATTTTC--TGCAGAAATTTGCAACTGACTGC 1490 1500 1510

ACTAACCT-TGAGTCAGAAAACAGAGAAAGGGTAATTTCCTT--TGCT-TCA----AATTCAAG-----GCCTT

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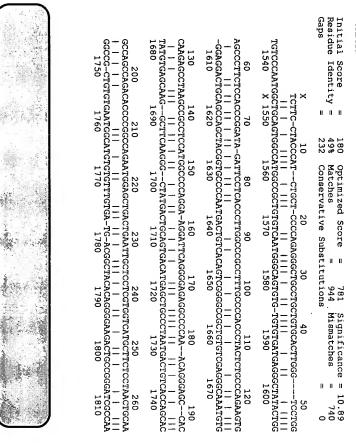
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Gherzi,R., Carnemolla,B., Siri,A., Ponassi,M. and Zardi,L.
Human Tenascin Gene: Structure of the 5' Region, Identification
Characterization of its Promoter Submitted (26-JUL-1994) to the EMBL/GenBank/DDBJ databases. Luciand Zardi, Call Biology Laboratory, Istituto Nazionale per la, Ricerca sul Cancro, Viale Benedetto XV, 10, Genova, 16132, Italy NCBI gi: 556844 Theria; Eutheria; Pr 1 (bases 1 to 7560) Zardi, L. Direct Submission Unpublished Eukaryota; Animalia; Metazoa; Chordata; Theria; Eutheria; Primates; Haplorhini; Homo sapiens human. tenascin-C; wnascin X78565 H.sapiens mRNA for (bases 1 to 7560) 3010 /translation="MGAMTQLIAGVFLAFLALIATEGGVLKKVIRHKROSGVNATLPEE
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polyA_signal BASE_COUNT_____1894 . ORIGIN 2019

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Page 2

ACT-TGCCTCTCATCCCTCGTGGGGCAGCTTTCTG-GACAGGTCCG---TCTCCTCCTTGGGGCCCTGCAGA

830 840 860

1220 CTACCAGO ACCA-C	1150 CACCCACC I TGAAGAGG 2700	1080 CAACCTCC 1 TGGTCTAG 2630	1010 CCCTCACG ATATGAAT 2560	940 GACCAAAT GA-GACAT 2490
1230 CCTCTTCTAJ TGCCTTGJ 2770	1160 TTGCCCACCA GTGACCACCA 2710	1090 AGCCTGGATA CTCCTGGGCA 2640	1020 CAGGACCCT- AAAGAAGATO 2570	950 CCCCGGATA(CTGTGGA-A(2500
1230 1230 1240 1250 1260 1270 1280 CTACCAGCCCTCTCTAAACACATCCTAC-ACCCACTCCCAGA ATCTGTCTCAGGAAGGGTAAGGTTC	1150 1160 1170 1180 1200 1210 CACCCACCTTGCCCACCCCTGGTCCAGCCTCCACCCCCTGCTGCTCCCACCCCACCC TGCACCCACCCTTGCTGCTCCACCCCCCCTGCTTCCTGCTCCAACGCCCACCCC	1080 1090 1100 1110 1120 1130 1140 CAACCTCCAGCCTGGATATTCTCCTTCCCCAACCCATCCTCCTACTG-GACAGTATACGCTCTTCCTTTC	1010 1020 1030 1050 1050 1070 CCCTCAGGCAGGCCCT-AGGACCCCGGCACATTTCCTCAGGAACATCAGACAACACCTCCCTGCCACCCAC	940 950 960 970 980 990 1000 GACCAAATCCCCGGATACCTGAACAGGATACAGGA-ACTCTTGAATGGAACTCGTGGA-CTC-TTTCCTGGA
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1260 CCCAGA-ATC' GGCTGAGATC' 2800	1190 CCTGCTTCCTI CCAGCCAI	0 11 CCTCCTACTO GCACATAGTO 2670	1040 1 TTCCTCAGGAA AGCCTGAGG-A 2600	980 CTCTTGAATC
1270 TGTCTCAGGA CGATGGCATTG 2810	1200 GACCCTTCTG KGATCGAGGTG 2740	1120 1 TG-GACAGTAT 	1050 1 ACATCAGACAC AGGCCAGAGAC 0 2610	990 GAACTCGTG GAAACCTGG 254
0 AAGGGTA GAGCTGACCI 2820	0 1210 GCTCCAACGCC CAAAGATGTCA 2750	1130 1 TACGCTCTTCC 	1060 1 CAGGCTCCCTG CCTCTTACCGG	10 GA-CTC-TTT GAGATCATCT 0 255
1280 -AGGTTC FACGGCA	LO DCCACCC ACAGAC 2760	1140 CCTCTTC CCTGGCC	1070 IGCCACC GCAAAC	1000 TTCCTGGA CTTCCGGA



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12. US-08-223-263-2 (1-1795) MUSZP3 Mouse ZP3 g

JOURNAL MEDLINE COMMENT ACCESSION KEYWORDS Locus REFERENCE SOURCE DEFINITION TITLE AUTHORS ORGANISM of the mouse zona pellucida Dev. Biol. 127, 287-295 (1988) 88242926 sperm-binding protein.
Mus musculus (NIH Swiss) oocyte,
pZP3.2, and DNA, clone MZG I. Draft entry and computer-readable sequence [1] kindly submitted J.Dean, 09-AUG-1988. Mus musculus MUSZP3 1317 bp ss-mRNA Mouse ZP3 gene, encoding zon Molecular analysis of cDNA coding ט, Dean Ringuette, M.J., Chamberlin, M.E., Eukaryota; Animalia; Chordata; Eutheria; Rodentia; Myomorpha; 1 (bases 1 to 1317) M20026 complete cds. gene, encoding zona pellucida sperm-bind zona pellucida sperm-binding protein, Vertebrata; Mammalia; Muridae; Murinae. cDNA to Baur, A.W., for ZP3, mRNA, a sperm binding protein Sobieski, D.A. clones pZP3.1 and γģ

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/note="sperm-binding protein (ZP3)"

/codon_start=1 401 c 3 340 g

Chromosome 6.

Initial Score Residue Identity 177 49% 196 Conservative Substitutions Optimized Score Matches 576 704

Significance Mismatches

11 11

TACACCTGTCCTG-CTGCCTGCTGTGGAC--TTTAGCTTGGGAGAA--TGGAAAACCCCAGATGGAGGAGA-C 420

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GAGGAGAAACTGGCTTTCTCTCTCTCGCCTGATGGAGGAGAACTGGAATA-CTG-----AG-AAATCGGCTCC -GGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACCAGCTGTCCCCAGCAGAACCTCTCT 720 760

990

ACCAAAC-CTCCAGGTCCCTGGACCAAATCCCCGGATACC---TGAACAGGATACACGAACTCTT---940

1080

1090

1100

1.00 10

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Initial Score Residue Identity JOURNAL MEDLINE COMMENT FEATURES REFERENCE AUTHORS TITLE SOURCE ORGANISM DEFINITION ACCESSION KEYWORDS 1390 1460 US-08-223-263-2 (1-1795) ADRFIBA Adenovirus type 5 fiber protein 390 1400 1410 1420 1430 1440 1450 GCCCTGGTAAAAGGGATACACTTCAGAAAAGGGAATCATTTTTCACTGT-ACA-TTATAAACCTTCAGAA CATGGCCCCAGGAAGGATTCAGGGGAGGGGGGGGGCCAAACAGGGAGCCAGGCCAGA-CCAGACACCCCGGGCAGA COUNT source Adenovirus type 5 fiber prot M18369 1 (bases 1 to 2530)
1 (bases 1 to 2530)
1 (bases 1 to 2530)
2 (broboczek, J. and Jacrot, B.
The sequence of adenovirus fiber:
between serotypes 2 and 5
Virology 161, 549-554 (1987) capsid protein; fiber protein. Adenovirus type 5 DNA, clone p Mastadenovirus h5 ω Virology 161, 88072096 Viridae; ds-DNA nonenveloped viruses; Adenoviridae đđ 11 11 11 762 <u>1</u> upstream /codon start=1
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1000

GG-ATTGTTGGAGACAAACT--TCA-CTGCCTCAGCCAGAACTA--CTGGC--TCTGGGCTTCTGAAGTGGC

840

850

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Page 9

4

AGT---ATGGAGCT--GACTG-AATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAG--GCTAAC---190 AGTCACCTACGACAGTAATACCACC---460 GTTAACTTGCACCAGTG---X 700 210 480 710 220 -CAAA-AGGG-GTATCTTTTGTCTGGTAAAGCAGGCCA-A 490 20 720 230 500 240 510 40 -GCTGTCCA 50 750

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CCT-CACAGTGTCAGAAGGAAAGCTAGCC-----CTGCAAACATCAGGC---CCCCTC-ACCA-CCACCGA 950 960 970

AAAGTTACTGGA--GCCT--TGGGTTTTGATTCACAAGGCAATATGCAACTTAATGTAGCAGGA-GGA-GGACTAA AACTGGACAAGATTTCCTACTTCTCCTGAAACCCCAAAGCCCTGGTAAAAGGGATACA-CAGGACTGAAAAAG 1390 1400 1410

-CAACT-CA-CTGA-TT

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1480

1490

1500

1510

14. US-08-223-263-2 (1-1795)

DYGCCA1B Discopyge ommata Ca2+ channel alpha 1 subunit

ACCESSION KEYWORDS SOURCE DEFINITION DNA. Discopyge ommata Ca2+ channel alpha 1 subunit I12532 calcium channel alpha-1 subunit. Discopyge ommata (library: lambda ZAP) adult electric lobe, brain 6981 bp ds-DNA gene sequence.

ORGANISM Discopyge ommata

Chondrichthyes;

REFERENCE TITLE AUTHORS Eukaryota; Animalia; Chordata; Vertebrata; Elasmobranchii; Euselachii; Neoselachii. 1 (bases 1 to 6981) Horne, W.A., Ellinor, P.T., Inman, I., Zhou, M. Schwarz, T.L. Tsien, R.W.

JOURNAL MEDLINE marine ray Discopyge ommata Proc. Natl. Acad. Sci. U.S.J 93248175 Molecular diversity of Ca2+ channel alpha 1 subunits from 90, 3787-3791 (1993)

COMMENT FEATURES gi: 290386

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/tissue type="electric lot
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a 1670 c 1767 g 1686 lobe, brain'

1686 t

BASE COUNT

Initial Score 164 Optimized II 701 Significance

H

9.70





24

*%\.

Residue Identity =

Conservative Substitutions

847 Mismatches

Matches

330 340 350 360 370 380 390 400
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CACC----TGCTCCGAGGAAAGGTGCGTTTCCTGATGCTTGTAGGAGGGT---CCA--CCCTCTGCGTCAGG

CCATCTGGGAGAGTCGGTGCACCGATCGCAG-ACACAAG---CCCTATG-AAGGGTTCTGTGTCTTACGCTAA

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6670
 1350 1360 1370 1380 1390 1390 CCTGGGAGACACTG-GACA-AGATTTCCT--ACTTTCT-CCTGAAACC--CCTGGTAAAGC-GACA-CCA-CCTGGTAAAAC-GACA-CCA-CAGAGC-GAGTGAACACCGAGTTGCTGGAAGAAACTCTGACCTTCGAGGTGGCTGTCCCCCCCGCAGGTGAAGAAACTCTGACCTTCGAGGTGGCTGTCCCC
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                                                                                                                                      TGC-CACTACCGCCACCGG---CAGGTCCCCCAGGACTTCAT---CCTTCACCACCCAACCTCCGCAG-AGT
                                                                                                                                                                                                                                                                                                                                                                                              GCCCCTATGCTGGT-GGTGACAGCAGGCAGC-CAATGGGGACACGCATCAGCTCCGATCCCTACCTGGGGTT
                                                                                                                                                                                                                                    TACACAGGACTGAAAAGGGAATCATTTTTCACTGTACATTATAAACCTTCAGAAGCTATTTTTTTAAGCTAT
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6970
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                                                                                                                                                                                                                                                                                     6800
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l5. US-08-223-263-2 (1-1795) MMGLUD Murine GLUD mRNA for glutamate dehydrogenase

REFERENCE AUTHORS TITLE LOCUS
DEFINITION
ACCESSION
KEYWORDS SOURCE ORGANISM MMGLUD 2942 bp RNA ROD Murine GLUD mRNA for glutamate dehydrogenase. Mus musculus mouse GLUD gene; glutamate dehydrogenase. Theria; Eutheria; Ro Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Cheria; Rodentia; Myomorpha; Muridae; Murinae.

Tzimagiorgis, G. and Moschonas, N.K. Molecular cloning, structure and expression analysis of a full-length mouse brain glutamate dehydrogenase cDNA Biochim. Biophys. Acta 1089 (2), 250-253 (1991)

JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL Direct Submission
Submitted (17-DEC-1990) to the EMBL/GenBank/DDBJ databases.
Moschonas N.K., Institute of Molecular Biology and Biotechnology, 2 (bases 1 to 2942) Moschonas, N.K.

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FEATURES COMMENT

gı:

51081

Department of Biology, Univ. of Crete

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RGILKIIKPCNHVLSLSFPIRDDGSWEVIEGYRAQHSQHRTPCKGGIRYSTDVSVDE
VKALASLMTYKCAVVDVPFGGAKAGVKINFKNYTDNELEKITRFTYBELAKKGFIGPG
LDVPAADMSTGERENSWIADDTYASTIGHYDINHACVTGKPISQGGIHGHRASATGRGV
FHGIENFINEASYMSILGMTPGFGDKTFVVQGFGNVGLHSMRYLHRFGAKCVGVGESD 236..1750 GLAYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFKVYNEAGVTFT* APRVKAK I IAEGANGPTTP EADK I FLERN IMV IPD LY LNAGGVTVS Y FEWLKNLNHVS YGRLTFKYERD SNYHLLMS VQES LERKFGKHGGT I PVVPTAEFQDR I SGASEKD I VHS GSIWNPDGIDPKELEDFKLQHGSILGFPKAKVYEGSILEADCDILIPAASEKQLTKSN /gene="GLUD" /EC_number="1.4.1.3" /note="NCBI gi: 51082" /gene="GLUD" /evidence=experimental /chromosome="14" /codon_start=1

Residue Identity Initial Score BASE COUNT 775 159 46% 222 /product="glutamate dehydrogenase (NAD(P)+)"
711 c 736 g 720 t /gene="GLUD" /EC_number="1.4.1.3" Optimized Score Matches n u 738 892 Significance Mismatches 11 9.33 793 0

GCAAGGCTAACG-CTGTCCAGCCCGGCTCCT-----CCTGCTTGTGAC-CTCCGAGTCCTCAGTAAACTG-CT

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J. J.Y.

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-CCCGGATACCTGAACAGGATACACGAACTCT----TGAATGGAACTC-GT-GGACTC-TTTCCTGGACCCT

TTGAGTCAGAAAACAGAGAAAGGGTAATTTCC-TTTG--CTTCAAAT---TCAAGGCCTT---CCAACGCCC

GTTCTTGTGACTCATTA-GTTA-ACGGACACTGTTCTGAA--CAAGTCAGTTGGAATCAGCCCCTTAAGAGA

Tue Apr 11 13:28:26 1995

Listing for Mary Hale

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maryh@stic

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